

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:21:54 ; Search time 45.33 Seconds

(Without alignments)
178.061 Million cell updates/sec

Title: US-09-351-778a-12

Sequence: 1 MGGSTAPTYDYRNTATGL.....NEKIHRLDGLKPCSLLDGYD 84

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 283138 segs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR.71.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	22.6	93	1 ERAD53	early E3A 10.5K pr
2	7	8.3	160	2 C95415	hypothetical prote
3	7	8.3	193	2 AG0186	probable sideropho
4	7	8.3	197	2 C86523	CFI42 hypothetical
5	7	8.3	387	2 C89783	hypothetical prote
6	7	8.3	391	2 D97201	alCR transformla
7	7	8.3	425	2 AC3909	MFS permease (lipo
8	7	8.3	459	2 C87534	hypothetical prote
9	7	8.3	487	2 B97684	probable tartrate
10	7	8.3	495	2 H71933	hypothetical prote
11	7	8.3	495	2 D64578	conserved hypotet
12	7	8.3	536	2 T72668	hypothetical prote
13	7	8.3	891	2 T36423	hypothetical prote
14	7	8.3	1175	2 H83437	probable large, mu
15	7	7.1	82	2 D82630	hypothetical prote
16	7	7.1	83	2 D82744	hypothetical prote
17	7	7.1	89	2 D87338	hypothetical prote
18	7	7.1	89	2 B26239	hypothetical prote
19	7	7.1	94	2 D82626	phage-related prot
20	7	7.1	97	2 I79265	phage-related prot
21	7	7.1	97	2 T40639	hypothetical prote
22	7	7.1	113	2 C81230	hypothetical prote
23	7	7.1	113	2 G81990	hypothetical prote
24	7	7.1	115	2 B64637	hypothetical prote
25	7	7.1	119	2 H83186	hypothetical prote
26	7	7.1	121	1 U01646	nucleic acid-bind
27	7	7.1	126	1 D95915	hypothetical prote
28	7	7.1	130	2 E70353	hypothetical prote
29	6	7.1	131	2 T25687	hypothetical prote

30	6	7.1	134	2 S52546	Ublonin variant Th
31	6	7.1	136	2 T23996	hypothetical prote
32	6	7.1	142	2 S32960	hypothetical prote
33	6	7.1	144	2 AE3588	high-affinity bran
34	6	7.1	148	2 T03569	hypothetical 16.9K
35	6	7.1	149	2 AG2708	conserved hypotet
36	6	7.1	150	2 G87270	general secretion
37	6	7.1	151	2 D64319	probable format d
38	6	7.1	157	2 S75191	hypothetical prote
39	6	7.1	157	2 S35037	helix-loop-helix p
40	6	7.1	157	2 T46683	hypothetical prote
41	6	7.1	160	2 D83755	hypothetical prote
42	6	7.1	170	2 T17286	hypothetical prote
43	6	7.1	172	2 F83337	probable sigma-70
44	6	7.1	174	2 T21945	hypothetical prote
45	6	7.1	177	2 F87600	conserved hypotet

ALIGNMENTS

RESULT 1
ERAD53
early E3A 10.5K protein - human adenovirus 5
C:Species: Mastadenovirus h5 (human adenovirus 5)
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C:Accession: A05245
R:Cladarias, C.; Mold, W.S.M.
Virology 140, 28-43, 1985
A:Title: DNA sequence of the early E3 transcription unit of adenovirus 5.
A:Reference number: A94335; MUID:85092388
A:Accession: A05245
A:Molecule type: DNA
A:Residues: 1-93 <CLN>
A:Cross-References: GB:X03002; NID:958503; PIDN:CA26784.1; PID:958507
C:Superfamily: adenovirus early E3A 10.5K protein
C:Keywords: early protein; transmembrane protein

Query Match 22.6%; Score 19; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 IALMEVCLIIIMILICLKR 47
DB 39 IALMFVCLIIIMILICLKR 57

RESULT 2

C95415
hypothetical protein Sma2279 (imported) - Sinorhizobium meliloti (strain 1021) magap1
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95415
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95415
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <CUR>
A:Cross-References: GB:AE006469; PIDN:AK65885.1; PID:914524394; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
beault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma2279
A:Genome: plasmid

Query Match 8.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
Db 28 TGSTIAP 34

RESULT 3
AC0186
probable siderophore biosynthetic enzyme alcB [Imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AC0186
R:Parikh, J.; Wren, B.W.; Thomson, N.R.; Tjball, R.W.; Holden, M.T.G.; Prentice, M.B.
dene-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Status: preliminary
A:Accession: AC0186
A:Molecule type: DNA
A:Residues: 1-193 <KUR>
A:Cross-references: GB:AL590842; PIDN:CMC90354.1; PID:q15979574; GSPDB:GN00175
C:Genetics:
A:Gene: alcB

Query Match 8.3%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 NEKIHRL 71
Db 149 NEKIHRL 155

RESULT 4
C86523
CT142 hypothetical protein_2 [Imported] - Chlamydomonas pneumoniae (strain J138)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86523
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2316, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: AB4491; MUID:20330349
A:Accession: C86523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:BA000008; MUID:98978632; PIDN:BA98469.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0259

Query Match 8.3%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
Db 74 ATGLTSA 80

RESULT 5
C89783
hypothetical protein SA0200 [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89783
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
me, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogatawara, N.; Hayashi, H.; Hiratsuka, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: C89783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:BA000018; PID:q13700123; PIDN:BB41422.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0200

Query Match 8.3%; Score 7; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LTSALNL 26
Db 27 LTSALNL 33

RESULT 6
D97201
aCAR transformylase domain of PurH-like protein [Imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97201
R:Noll, M.J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: AB9900; MUID:21359325; PMID:21359325
A:Accession: D97201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80399.1; PID:q15025462; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CMC2445

Query Match 8.3%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
Db 58 ATGLTSA 64

RESULT 7
AC2909
MFS permease [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AC2909
R:Wood, D.W.; Sedubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo
erage, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCl
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Author: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AC2909
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-425 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AA143689.1; PID:917741216; GSPDB:GN00186
 A:Experimental source: strain C58 (DuPont)
 C:Genetics:
 A:Gene: Atu2708
 A:Map position: circular chromosome

Query Match 8.3%; Score 7; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 TGSTAP 8
 DB 390 TGSTAP 396

RESULT 8
 C87534
 hypothetical protein CC2300 [imported] - *Caulobacter crescentus*
 C:Species: *Caulobacter crescentus*
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: C87534
 R:Name: W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 n, J.; Land, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: C87534
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-459 <STO>
 A:Cross-references: GB:AE005673; NID:g13423819; PIDN:NAK24271.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2300
 C:Superfamily: Arabidopsis 2-dehydro-3-deoxyheptonate aldolase 1

Query Match 8.3%; Score 7; DB 2; Length 459;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 60 VLNPHNE 66
 DB 308 VLNPHNE 314

RESULT 9
 B97684
 Probable taurate transporter AGR_C4908 [imported] - *Agrobacterium tumefaciens* (strain
 C:Species: *Agrobacterium tumefaciens*
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: B97684
 R:Gooder, B.; Hinkle, G.; Gitting, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A:Reference number: A97359; PMID:11743194
 A:Accession: B97684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-487 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK8427.1; PID:g15157922; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C4908

A:Map position: circular chromosome

Query Match 8.3%; Score 7; DB 2; Length 487;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 TGSTAP 8
 DB 452 TGSTAP 458

RESULT 10
 H71933
 hypothetical protein jhp0420 - *Helicobacter pylori* (strain J99)
 C:Species: *Helicobacter pylori*
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
 C:Accession: H71933
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.
 i Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
 A:Reference number: A71800; MUID:99120557
 A:Accession: H71933
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-495 <ARN>
 A:Cross-references: GB:AE001476; GB:AE001439; NID:g4154949; PIDN:AAD06001.1; PID:g4415
 C:Genetics:
 A:Gene: jhp0420
 C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0420

Query Match 8.3%; Score 7; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 26 LPOIALM 32
 DB 467 LPOIALM 473

RESULT 11
 D64578
 conserved hypothetical protein HP0468 - *Helicobacter pylori* (strain 26695)
 C:Species: *Helicobacter pylori*
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000
 C:Accession: D64578
 R:Tomb, J.F.; White, O.; Krlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKe
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Meldman, J.M.; Fujii, C.; Bowman, C.; Watney,
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser,
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A:Reference number: A64520; MUID:97394467
 A:Accession: D64578
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-495 <TOM>
 A:Cross-references: GB:AE000561; GB:AE000511; NID:g2313564; PIDN:AAD07530.1; PID:g231
 C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0420

Query Match 8.3%; Score 7; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 26 LPOIALM 32
 DB 467 LPOIALM 473

RESULT 12

T27668

hypothetical protein ZK1053.2 - *Caenorhabditis elegans*A:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T27668

R:Kershaw, J.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z20402

A:Accession: T27668

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-536 <WIL>

A:Cross-references: EMBL:Z82084; PIDN:CA804976.1; GSPDB:GN00019; CESP:ZK1053.2

A:Experimental source: clone ZK1053

C:Genetics:

A:Gene: CESP:ZK1053.2

A:Map position: 1

A:Inserts: 56/3; 88/3; 203/1; 228/2; 383/1; 467/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK1053.2

Query Match 8.3%; Score 7; DB 2; Length 536;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 STIAPTT 10

DB 295 STIAPTT 301

RESULT 13

T36423

probable large, multifunctional secreted protein - *Streptomyces coelicolor* (fragment)C:Species: *Streptomyces coelicolor*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36423

R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, September 1999

A:Reference number: Z21606

A:Accession: T36423

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-891 <SAU>

A:Cross-references: EMBL:AL10974; PIDN:CA853335.1; GSPDB:GN00070; SCOEDB:SCF34.24

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCF34.24

Query Match 8.3%; Score 7; DB 2; Length 891;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 RLDGLKP 76

DB 628 RLDGLKP 634

RESULT 14

H83437

hypothetical protein PA1669 [imported] - *Pseudomonas aeruginosa* (strain PA01)C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83437

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laribay, K.; Llm,

Nature 406: 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: H83437

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1175 <STO>
 A:Cross-references: GB:AE004594; GB:AE004091; NID:g9947630; PIDN:MAC05058.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1669

Query Match 8.3%; Score 7; DB 2; Length 1175;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRARP 52

DB 213 KRRARP 219

RESULT 15

D82630

hypothetical protein XF1852 [imported] - *Xylella fastidiosa* (strain 9a5c)C:Species: *Xylella fastidiosa*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82630

R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq

Nature 406: 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82630

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-82 <SIM>

A:Cross-references: GB:AE004006; GB:AE003849; NID:g9106932; PIDN:AF84658.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kurame, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri,

Rodrigues, V.; Rosa, A.C. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1852

Query Match 7.1%; Score 6; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 KPCLSL 80

DB 32 KPCLSL 37

Search completed: June 21, 2002, 08:21:55
 Job time: 100 sec

